

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/010,065

DATE: 12/20/2001
TIME: 21:04:14

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\12202001\J010065.raw

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4 <110> APPLICANT: Allen, Keith D.
5     Matthews, William
6     Moore, Mark
8 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GLUCAGON
9     RECEPTOR GENE DISRUPTIONS
12 <130> FILE REFERENCE: R-648
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/010,065
C--> 15 <141> CURRENT FILING DATE: 2001-12-05
17 <150> PRIOR APPLICATION NUMBER: US 60/251,804
18 <151> PRIOR FILING DATE: 2000-12-06
20 <150> PRIOR APPLICATION NUMBER: US 60/266,044
21 <151> PRIOR FILING DATE: 2001-02-01
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1944
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus musculus
32 <400> SEQUENCE: 1
33 cagggtctcc ctgcacacct gaggagaggt gcacacactc tgaggaccta ggtgtgcaac 60
34 ctctgccaga tgtggggcgt ggctacccag aggcattgccc ctcacccagc tccactgtcc 120
35 ccacctgctg ctgctgctgt tggctgctgtc atgtctgcca gaggcacccct ctgcccaggt 180
36 aatggacttt ttgttgaga agtggaaagct ctatagtac caatgtcacc acaacctaag 240
37 cctgctgccc ccacctactg agctggctgt taacagaacc ttgcacaact actcctgctg 300
38 gcctgacacc cctcccaaca ccactgccaa catttcctgc ccctggtaacc taccttggtg 360
39 ccacaaaatgt cagcaccggc tagtgttcaa gaggtgtggg cccgatgggc agtgggttcg 420
40 agggccacgg gggcagccgt ggccaaacgc ctcccaatgt cagttggatg atgaagagat 480
41 cgagggtccag aagggggtgg ccaagatgtt tagcagccag caggtgatgt acaccgtggg 540
42 ctacagtctg tccctggggg cttgtctcct tgcgctggtc atcctgctgg gcctcaggaa 600
43 gctgcactgc acccgaaaact acatccatgg gaacctgtt gcttccttg tgctcaaggc 660
44 tggctctgtg ttggtcatcg attggctgtc gaagacacgg tacagccaga agattggcga 720
45 tgacctcagt gtgagcgtct ggctcgtga cggggcgatg gcccgtgca gagtggccac 780
46 agtgatcatg cagtaacggca tcatacccaa ctattgttgg ttgctggtag agggcgtgt 840
47 cctgtacagc ctgctgagcc ttgccacccct ctctgagagg agcttcttt ccctctaccc 900
48 gggcattggc tggggtgcgc ccctgctgtt tgtcatcccc tgggtggtag tcaagtgtct 960
49 gtttggaaat gttcagtgtc ggaccagcaa tgacaacatg ggattctgtt ggatccgtcg 1020
50 tattcctgtc ttccctggcct tactgtatcaa ttttttcattc ttgtccaca tcattcaact 1080
51 tcttggcc aagctgcgtg cccatcagat gcactatgtc gattacaagt tccggctggc 1140
52 caggtccacg ctgacccctca tccctctgtt ggggtccac gaggtggctt ttgcctttgt 1200
53 gactgacgag catgccaag gcaccctgcg ctccaccaag ctctttttt acctgttcc 1260
54 cagctcccttc cagggctgtc tgggtggctgt tctctactgt ttcctcaaca aggaggtgca 1320
55 ggcagagctg atgcggcggtt ggaggcaatg gcaagaaggc aaagctcttc aggagggaaag 1380
56 gttggccagc agccatggca gccacatggc cccagcaggc cttgtcatg gtatccctg 1440
57 tgagaaactt cagcttatga gtgcaggcag cagcagtggg actggctgtg tgccctctat 1500
58 ggagacctcg ctggccagta gtctcccaag gttggctgac agccccacccatc gaatctccac 1560
59 ttggagccta ggcagggtgtt gttcaagaaa gggccctcaga ggacaaccca gagccagatg 1620
60 cccggccaag gttgaagagc caaagcagca agacagcagc ttgtactgtg cacactcccc 1680

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61 taacctgtcc tagcctggca caggccacag tgacagagta ggggttggat atgatggaga 1740
62 agccatgtta tctatgaact ctgagtgttc ccatgtgtgt tgacatggtc cctgtaccca 1800
63 gatatgtcct tcagtaaaaaa gtcgagtgg agctgctgca cagctcggtt acagcaggct 1860
64 tgaagcccccc agggacgggg tttgggaggg cggggatgag cagcacactc agcaggtgga 1920
65 gcgcgttgtc aaccaggaa agaa 1944
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 485
69 <212> TYPE: PRT
70 <213> ORGANISM: Mus musculus
72 <400> SEQUENCE: 2
73 Met Pro Leu Thr Gln Leu His Cys Pro His Leu Leu Leu Leu Leu Leu
74   1           5           10          15
75 Val Leu Ser Cys Leu Pro Glu Ala Pro Ser Ala Gln Val Met Asp Phe
76     20          25          30
77 Leu Phe Glu Lys Trp Lys Leu Tyr Ser Asp Gln Cys His His Asn Leu
78     35          40          45
79 Ser Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp
80     50          55          60
81 Asn Tyr Ser Cys Trp Pro Asp Thr Pro Pro Asn Thr Thr Ala Asn Ile
82 65           70          75          80
83 Ser Cys Pro Trp Tyr Leu Pro Trp Cys His Lys Val Gln His Arg Leu
84     85          90          95
85 Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg
86     100         105         110
87 Gly Gln Pro Trp Arg Asn Ala Ser Gln Cys Gln Leu Asp Asp Glu Glu
88     115         120         125
89 Ile Glu Val Gln Lys Gly Val Ala Lys Met Tyr Ser Ser Gln Gln Val
90     130         135         140
91 Met Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala
92 145           150         155         160
93 Leu Val Ile Leu Leu Gly Leu Arg Lys Leu His Cys Thr Arg Asn Tyr
94     165         170         175
95 Ile His Gly Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Gly Ser Val
96     180         185         190
97 Leu Val Ile Asp Trp Leu Leu Lys Thr Arg Tyr Ser Gln Lys Ile Gly
98     195         200         205
99 Asp Asp Leu Ser Val Ser Val Trp Leu Ser Asp Gly Ala Met Ala Gly
100    210         215         220
101 Cys Arg Val Ala Thr Val Ile Met Gln Tyr Gly Ile Ile Pro Asn Tyr
102 225           230         235         240
103 Cys Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Ser Leu Leu Ser Leu
104     245         250         255
105 Ala Thr Phe Ser Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly
106     260         265         270
107 Trp Gly Ala Pro Leu Leu Phe Val Ile Pro Trp Val Val Val Lys Cys
108     275         280         285
109 Leu Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe
110     290         295         300
111 Trp Trp Ile Leu Arg Ile Pro Val Phe Leu Ala Leu Leu Ile Asn Phe

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112 305           310           315           320
113 Phe Ile Phe Val His Ile Ile Gln Leu Leu Val Ala Lys Leu Arg Ala
114           325           330           335
115 His Gln Met His Tyr Ala Asp Tyr Lys Phe Arg Leu Ala Arg Ser Thr
116           340           345           350
117 Leu Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe
118           355           360           365
119 Val Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Thr Lys Leu Phe
120           370           375           380
121 Phe Asp Leu Phe Leu Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu
122 385           390           395           400
123 Tyr Cys Phe Leu Asn Lys Glu Val Gln Ala Glu Leu Met Arg Arg Trp
124           405           410           415
125 Arg Gln Trp Gln Glu Gly Lys Ala Leu Gln Glu Glu Arg Leu Ala Ser
126           420           425           430
127 Ser His Gly Ser His Met Ala Pro Ala Gly Pro Cys His Gly Asp Pro
128           435           440           445
129 Cys Glu Lys Leu Gln Leu Met Ser Ala Gly Ser Ser Gly Thr Gly
130           450           455           460
131 Cys Val Pro Ser Met Glu Thr Ser Leu Ala Ser Ser Leu Pro Arg Leu
132 465           470           475           480
133 Ala Asp Ser Pro Thr
134           485
137 <210> SEQ ID NO: 3
138 <211> LENGTH: 200
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Targeting Vector
145 <400> SEQUENCE: 3
146 gcagccgtgg cgcaacgcct cccaatgtca gttggatgat gaagagatcg aggtccaggt 60
147 cagctctgga gggtatgggg tggtgtcaca gcggggctgt gtggggccag gggatacggc 120
148 actgcccagc cccactcggc ctctggttt cagaaggggg tggccaagat gtatagcagc 180
149 cagcaggtga cgtacaccgt
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 200
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Targeting Vector
159 <400> SEQUENCE: 4
160 gaggtggct ttgcctttgt gactgacgag catgcccag gcaccctgcg ctccaccaag 60
161 ctctttttt acctgttcct cagctccttc caggtgagtc tccatcatc cccacccctg 120
162 ggacccagag tgctgtcctt gaccacttc tttctccagg gtctgctggt ggctgttctc 180
163 tactgtttcc tcaacaagga
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 2034
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens

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170 <400> SEQUENCE: 5
171 ggatctggca ggcgcgcgaa gacgagcggt caccggcgcc cgaccggagc gcgcccagag 60
172 gacggcgaaa agccaagccg acccccggc agcgcggcgc gggccctgag gctcaaagg 120
173 gcagcttcag gggaggacac cccactggcc aggacgcccc aggctctgt gctctgccac 180
174 tcagctgccc tcggaggagc gtacacacac accaggactg cattgccccca gtgtgcagcc 240
175 cctgcccagat gtggggaggca gctagctgcc cagaggcatg ccccccgtcc agccacagcg 300
176 acccctgctg ctgttgcgtc tgctgctggc ctgcccagcca caggtccccct ccgctcagg 360
177 gatggacttc ctgtttgaga agtggaaagt ctacgggtac cagtgtaacc acaacactgag 420
178 cctgctgccc cctccacgg agctgggtgtg caacagaacc ttgcacaagt attcctgctg 480
179 gcccggacacc cccgccaata ccacggccaa catccctgc ccctggtacc tgcctggca 540
180 ccacaaagtg caacaccgct tcgtttcaaa gagatgcggg cccgacggc agtgggtgcg 600
181 tggaccccg gggcagcctt ggcgtgatgc ctcccagtgc cagatggatg gcgaggagat 660
182 tgaggtccag aaggagggtgg ccaagatgta cagcagctt caggtgtatgt acacagtggg 720
183 ctacagcctg tccctggggg ccctgctctt cgccttggcc atcctggggg gcctcagcaa 780
184 gtcgactgc acccgcaatg ccattcacgc gaatctgttt gcgtccttc tgctgaaagc 840
185 cagctccgtg ctggtcattt atgggctgtt caggacccgc tacagccaga aaattggcga 900
186 cgacctcagt gtcagcacct ggctcagtga tggagcgggtg gctggctgcc gtgtggccgc 960
187 ggtttcatg caatatggca tcgtggccaa ctactgctgg ctgctgggtt agggcctgtt 1020
188 cctgcacaac ctgctggcc tggccaccc ccccgagagg agttctca gcctctaccc 1080
189 gggcatcggc tgggggtggcc ccatgctgtt cgtcgcccc tggcagttgg tcaagtgtct 1140
190 gttcgagaac gtccagtgtt ggaccagcaa tgacaaatcg ggcttctgtt ggatcctgcg 1200
191 gttccctgtc ttccctggcca tcctgatcaa ctttttcattc ttcgccgca tcgttcatgt 1260
192 gtcgtggcc aagctcgaaa cacggcagat gcaccacaca gactacaagt tccggctggc 1320
193 caagtccacg ctgaccctca tccctctgtt gggcgtccac gaagtggctt ttgccttcgt 1380
194 gacggacgag cacgcccagg gcaccctgcg ctccgccaag ctcttcttcg acctttccct 1440
195 cagctccccc caggccctgc ttgggtgtt cctctactgc ttccctcaaca aggaggtgca 1500
196 gtcggagctg cggcggcggtt ggcaccgcgt ggcctggc aaagtgttat gggaggagcg 1560
197 gaacaccagc aaccacaggc cctcatcttc gcccggccac ggcctccca gcaaggagct 1620
198 gcagtttggg aggggtgggtg gcagccagga ttcatctgcg gagacccctt tggctgggtgg 1680
199 cctccctaga ttgggtgaga gccccttcg aaccctgctg ggaccccaagc tagggctgg 1740
200 ctctggcacc cagagggcgtc gtcggacaac ccagaactgg acgcccagct gaggctgggg 1800
201 gcggggggagc caacagcgc ccccacctac ccccccaccc cagtgtggct gtctgcgaga 1860
202 ttgggcctcc tctccctgca cctgccttgtt ccctgggtca gaggtgagca gaggagtcca 1920
203 gggcgggagt gggggctgtg cctgtgaactg cgtgccagtg tcccccacgt tgcggcacg 1980
204 tcccatgtgc atggaaatgt cctccaaacaa taaagagctc aagtggtcac cgtg 2034
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 477
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 6
212 Met Pro Pro Cys Gln Pro Gln Arg Pro Leu Leu Leu Leu Leu Leu
213 1 5 10 15
214 Leu Ala Cys Gln Pro Gln Val Pro Ser Ala Gln Val Met Asp Phe Leu
215 20 25 30
216 Phe Glu Lys Trp Lys Leu Tyr Gly Asp Gln Cys His His Asn Leu Ser
217 35 40 45
218 Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp Lys
219 50 55 60
220 Tyr Ser Cys Trp Pro Asp Thr Pro Ala Asn Thr Thr Ala Asn Ile Ser

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221	65	70	75	80
222	Cys Pro Trp Tyr Leu Pro Trp His His Lys Val Gln His Arg Phe Val			
223	85	90	95	
224	Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg Gly			
225	100	105	110	
226	Gln Pro Trp Arg Asp Ala Ser Gln Cys Gln Met Asp Gly Glu Glu Ile			
227	115	120	125	
228	Glu Val Gln Lys Glu Val Ala Lys Met Tyr Ser Ser Phe Gln Val Met			
229	130	135	140	
230	Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala Leu			
231	145	150	155	160
232	Ala Ile Leu Gly Gly Leu Ser Lys Leu His Cys Thr Arg Asn Ala Ile			
233	165	170	175	
234	His Ala Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Ser Ser Val Leu			
235	180	185	190	
236	Val Ile Asp Gly Leu Leu Arg Thr Arg Tyr Ser Gln Lys Ile Gly Asp			
237	195	200	205	
238	Asp Leu Ser Val Ser Thr Trp Leu Ser Asp Gly Ala Val Ala Gly Cys			
239	210	215	220	
240	Arg Val Ala Ala Val Phe Met Gln Tyr Gly Ile Val Ala Asn Tyr Cys			
241	225	230	235	240
242	Trp Leu Leu Val Glu Gly Leu Tyr Leu His Asn Leu Leu Gly Leu Ala			
243	245	250	255	
244	Thr Leu Pro Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly Trp			
245	260	265	270	
246	Gly Ala Pro Met Leu Phe Val Val Pro Trp Ala Val Val Lys Cys Leu			
247	275	280	285	
248	Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe Trp			
249	290	295	300	
250	Trp Ile Leu Arg Phe Pro Val Phe Leu Ala Ile Leu Ile Asn Phe Phe			
251	305	310	315	320
252	Ile Phe Val Arg Ile Val Gln Leu Leu Val Ala Lys Leu Arg Ala Arg			
253	325	330	335	
254	Gln Met His His Thr Asp Tyr Lys Phe Arg Leu Ala Lys Ser Thr Leu			
255	340	345	350	
256	Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe Val			
257	355	360	365	
258	Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Ala Lys Leu Phe Phe			
259	370	375	380	
260	Asp Leu Phe Leu Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu Tyr			
261	385	390	395	400
262	Cys Phe Leu Asn Lys Glu Val Gln Ser Glu Leu Arg Arg Arg Trp His			
263	405	410	415	
264	Arg Trp Arg Leu Gly Lys Val Leu Trp Glu Glu Arg Asn Thr Ser Asn			
265	420	425	430	
266	His Arg Ala Ser Ser Ser Pro Gly His Gly Pro Pro Ser Lys Glu Leu			
267	435	440	445	
268	Gln Phe Gly Arg Gly Gly Ser Gln Asp Ser Ser Ala Glu Thr Pro			
269	450	455	460	

VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date